

## SEQUENCE LISTING

&lt;110&gt; Advanced Technologies (Cambridge) Ltd

&lt;120&gt; Plant Limit Dextrinase Inhibitor

&lt;130&gt; RD-ATC-32

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 25

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 517

&lt;212&gt; DNA

&lt;213&gt; Hordeum vulgare

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (14) .. (457)

&lt;400&gt; 1

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gcc	gtc	ttg	ctc	tgc	gtc	ctc	gcc	gtc	gcc	gcc	acc	ctg	gag	agc	97
Ala	Val	Leu	Leu	Ser	Val	Leu	Ala	Val	Ala	Ala	Ala	Thr	Leu	Glu	Ser
	15					20						25			

gtc	aag	gac	gag	tgc	caa	cca	ggg	gtg	gac	ttc	ccg	cat	aac	ccg	tta	145
Val	Lys	Asp	Glu	Cys	Gln	Pro	Gly	Val	Asp	Phe	Pro	His	Asn	Pro	Leu	
	30					35					40					

gcc	acc	tgc	cac	acc	tac	gtg	ata	aaa	cgg	gtc	tgc	ggc	cgc	ggg	ccc	193
Ala	Thr	Cys	His	Thr	Tyr	Val	Ile	Lys	Arg	Val	Cys	Gly	Arg	Gly	Pro	
	45				50					55					60	

agc	cgg	ccc	atg	ctg	gtg	aag	gag	cgg	tgc	tgc	cgg	gag	ctg	gcg	gcc	241
Ser	Arg	Pro	Met	Leu	Val	Lys	Glu	Arg	Cys	Cys	Arg	Glu	Leu	Ala	Ala	
			65						70					75		

gtc	ccg	gat	cac	tgc	cgg	tgc	gag	gcg	ctg	cgc	atc	ctc	atg	gac	ggg	289
Val	Pro	Asp	His	Cys	Arg	Cys	Glu	Ala	Leu	Arg	Ile	Leu	Met	Asp	Gly	
			80					85					90			

gtg	cgc	acg	ccg	gag	ggc	cgc	gtg	gtt	gag	gga	cgg	ctc	ggg	gac	agg	337
Val	Arg	Thr	Pro	Glu	Gly	Arg	Val	Val	Glu	Gly	Arg	Leu	Gly	Asp	Arg	
		95					100					105				

cgt	gac	tgc	ccg	agg	gag	gag	cag	agg	gcg	ttc	gcc	gcc	acg	ctt	gtc	385
Arg	Asp	Cys	Pro	Arg	Glu	Glu	Gln	Arg	Ala	Phe	Ala	Ala	Thr	Leu	Val	
	110					115					120					

acg	gcg	gcg	gag	tgc	aac	cta	tgc	tcc	gtc	cag	gag	ccg	gga	gta	cgc	433
Thr	Ala	Ala	Glu	Cys	Asn	Leu	Ser	Ser	Val	Gln	Glu	Pro	Gly	Val	Arg	
	125				130					135					140	

ttg gtg cta ctg gca gat gga tga cgatcgaaat gcgccaaggt aatgaagcgg 487.  
 Leu Val Leu Leu Ala Asp Gly  
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agtactgtat acagaataaa agtactcgag 517

<210> 2

<211> 147

<212> PRT

<213> Hordeum vulgare

<400> 2

Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly Ala Val Leu Leu  
 1 5 10 15  
 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu  
 20 25 30  
 Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His  
 35 40 45  
 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met  
 50 55 60  
 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His  
 65 70 75 80  
 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro  
 85 90 95  
 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro  
 100 105 110  
 Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu  
 115 120 125  
 Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg Leu Val Leu Leu  
 130 135 140  
 Ala Asp Gly  
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<210> 3

<211> 672

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (39)..(482)

<400> 3

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 cgc ttc gtc ctc tcc ggc gcc gtc ttg ctc tcg gtc ctc gcc gtc gcc 104  
 Arg Phe Val Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala Val Ala  
 10 15 20  
 gcc gcc acc ttg gag agc gtc aag gac gag tgc caa cta ggg gtg gac 152  
 Ala Ala Thr Leu Glu Ser Val Lys Asp Glu Cys Gln Leu Gly Val Asp  
 25 30 35  
 ttc ccg cat aac ccg tta gcc acc tgc cac acc tac gtg ata aaa cgg 200  
 Phe Pro His Asn Pro Leu Ala Thr Cys His Thr Tyr Val Ile Lys Arg  
 40 45 50

gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg tgc 248  
 Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg Cys  
 55 60 65 70

tgc cgg gag ctg gcg gcc gtc ccg gat cac tgc cgg tgc gag gcg ctg 296  
 Cys Arg Glu Leu Ala Val Pro Asp His Cys Arg Cys Glu Ala Leu  
 75 80 85

cgc atc ctc atg gac ggg gtg cgc acg ccg gag ggc cgc gtg gtt gag 344  
 Arg Ile Leu Met Asp Gly Val Arg Thr Pro Glu Gly Arg Val Val Glu  
 90 95 100

gga cgg ctc ggt gac agg cgt gac tgc ccg agg gag gag cag agg gcg 392  
 Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala  
 105 110 115

ttc gcc gcc acg ctt gtc acg gcg gcg gag tgc aac cta tcg tcc gtc 440  
 Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Ser Ser Val  
 120 125 130

cag gcg ccg gga gta cgc ttg gtg cta ctg gca gat gga tga 482  
 Gln Ala Pro Gly Val Arg Leu Val Leu Leu Ala Asp Gly  
 135 140 145

cgatgcaaat gcgccaaggt aatgaagcgg agtactgtat acagaataaaa agtactcgag 542

tgaaaacaaa ctcataaata aacottgtga gatgtatgcg tatgatctat ggtgtggaca 602

gttaaattgt ggccgattga tgaataaaaa aggttgaac aaattaaatt gttgtggggtt 662

catatactat 672

<210> 4

<211> 147

<212> PRT

<213> Hordeum vulgare

<400> 4

Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly Ala Val Leu Leu  
 1 5 10 15  
 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu  
 20 25 30  
 Cys Gln Leu Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His  
 35 40 45  
 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met  
 50 55 60  
 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His  
 65 70 75 80  
 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro  
 85 90 95  
 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro  
 100 105 110  
 Arg Glu Glu Gln Arg Ala Phe Ala Thr Leu Val Thr Ala Ala Glu  
 115 120 125  
 Cys Asn Leu Ser Ser Val Gln Ala Pro Gly Val Arg Leu Val Leu Leu  
 130 135 140  
 Ala Asp Gly  
 145

<210> 5  
 <211> 621  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> CDS  
 <222> (45)..(506)

<400> 5

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                                         1

cat cgt cgc ttc ctc ctc tcc ggc gcc gtc ttg ctc tca gtc ctc gcc 104
His Arg Arg Phe Leu Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala
  5                      10                      15                      20

gcc gtg gcc gcc ctg gag agc gtt gag gac gag tgc cag cca ggg gtg 152
Ala Val Ala Ala Leu Glu Ser Val Glu Asp Glu Cys Gln Pro Gly Val
                      25                      30                      35

gcc ttc ccg cac aac gca tta gcc acc tgc cac acc tac gtg atc aaa 200
Ala Phe Pro His Asn Ala Leu Ala Thr Cys His Thr Tyr Val Ile Lys
                      40                      45                      50

cgg gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg 248
Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg
                      55                      60                      65

tgt tgc cgg gag ctg gcg gtc gtc ccg gat tac tgc cgg tgc gag gca 296
Cys Cys Arg Glu Leu Ala Val Val Pro Asp Tyr Cys Arg Cys Glu Ala
                      70                      75                      80

ctg cgc gtc ctc atg gat ggg gtg cgc gcg gag gag ggc cac gtg gtg 344
Leu Arg Val Leu Met Asp Gly Val Arg Ala Glu Glu Gly His Val Val
                      85                      90                      95                      100

gag ggc cgc ctt ggt gac aga cgt gac tgc ccg agg gag gcg cag cgg 392
Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg Glu Ala Gln Arg
                      105                      110                      115

gag ttc gcc gcc acg ctg gtc acg gcg gcg gag tgc aac ctg ccg acc 440
Glu Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Pro Thr
                      120                      125                      130

gtc tcg gga gtc ggg agt aca ctt ggt gcg acc ggc aga tgg atg acg 488
Val Ser Gly Val Gly Ser Thr Leu Gly Ala Thr Gly Arg Trp Met Thr
                      135                      140                      145

atc gaa ttg ccc aag taa tgaagcgatc aagcgaagta ctctactggc 536
Ile Glu Leu Pro Lys
150

agatggagta ctgcatgtag aataaaaagta ctcaagtga aacaaataaa taaagcttgt 596

gagctgtatg cgtatgaaaa aaaaa 621

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<210> 6  
 <211> 153  
 <212> PRT  
 <213> Triticum aestivum

<400> 6  
 Met Ala Ser Asn His Arg Arg Phe Leu Leu Ser Gly Ala Val Leu Leu  
   1                  5                  10                  15  
 Ser Val Leu Ala Ala Val Ala Ala Leu Glu Ser Val Glu Asp Glu Cys  
           20                  25                  30  
 Gln Pro Gly Val Ala Phe Pro His Asn Ala Leu Ala Thr Cys His Thr  
           35                  40                  45  
 Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu  
       50                  55                  60  
 Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Val Val Pro Asp Tyr Cys  
       65                  70                  75                  80  
 Arg Cys Glu Ala Leu Arg Val Leu Met Asp Gly Val Arg Ala Glu Glu  
                   85                  90                  95  
 Gly His Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg  
                   100                  105                  110  
 Glu Ala Gln Arg Glu Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys  
           115                  120                  125  
 Asn Leu Pro Thr Val Ser Gly Val Gly Ser Thr Leu Gly Ala Thr Gly  
       130                  135                  140  
 Arg Trp Met Thr Ile Glu Leu Pro Lys  
       145                  150

<210> 7  
 <211> 444  
 <212> DNA  
 <213> Hordeum spontaneum

<220>  
 <221> CDS  
 <222> (1)..(444)

<400> 7  
 atg gcg ttc aag tac cag ctc ctc ctc tcg gcc gcc gtc atg ctc gcc 48  
 Met Ala Phe Lys Tyr Gln Leu Leu Leu Ser Ala Ala Val Met Leu Ala  
   1                  5                  10                  15  
 att ctc gcc gcc act gtc acc agt ttc ggg gat atg tgt gct cca ggg 96  
 Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly  
           20                  25                  30  
 gat gcg ttg cca gcc aac cct ctc aga gcc tgc cgc acc tat gtg gtt 144  
 Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val  
       35                  40                  45  
 agt caa atc tgc cat gta ggc cct aga cta tcc acc tgg gac atg aag 192  
 Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys  
       50                  55                  60  
 agg cgg tgc tgc gac gag ctg tcg gcc atc ccg gcg tac tgc aga tgc 240  
 Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys  
       65                  70                  75                  80

gag gcg ctg cgt atc atc atg gat ggg aca gta act tgg cag ggt gtg 288  
 Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val  
                     85                    90                    95  
  
 ttc ggt gcc tac ttc aag gac atg ccc aac tgc cct agg gtg atg caa 336  
 Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln  
                     100                    105                    110  
  
 acg agc tac gcc gcc aac ctc gtc aac ccg cag gag tgc aac cta tgg 384  
 Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp  
                     115                    120                    125  
  
 act atc cac ggc agc ccg tcc tgc ccc gaa ctg cag ccc gga tat gaa 432  
 Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu  
                     130                    135                    140  
  
 gtg gtc ttg taa  
 Val Val Leu 444  
 145

<210> 8  
 <211> 147  
 <212> PRT  
 <213> Hordeum spontaneum

<400> 8  
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   1                    5                    10                    15  
 Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly  
                     20                    25                    30  
 Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val  
                     35                    40                    45  
 Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys  
                     50                    55                    60  
 Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys  
                     65                    70                    75                    80  
 Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val  
                     85                    90                    95  
 Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln  
                     100                    105                    110  
 Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp  
                     115                    120                    125  
 Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu  
                     130                    135                    140  
 Val Val Leu  
 145

<210> 9  
 <211> 483  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> CDS  
 <222> (1)..(483)

<400> 9

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Met Ala Ser Asn Lys Val Val Phe Ser Val Leu Leu Leu Ala Val Val
1 5 10 15

tcc gtg ctc gcg gcg acg gcg acc atg gcg gag tac cac cac caa gac 96
Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp
20 25 30

cag gtg gtc tac acc ccg ggc ccg ctc tgt cag cca gga atg ggc tac 144
Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr
35 40 45

ccg atg tac ccg ctc ccg cgt tgc cgg gcg ttg gtg aag cgc cag tgc 192
Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys
50 55 60

gtc ggc cgt ggc acg gcc gcc gcc gcc gag cag gtc cgg cga gac tgc 240
Val Gly Arg Gly Thr Ala Ala Ala Ala Glu Gln Val Arg Arg Asp Cys
65 70 75 80

tgc cgg cag ctc gcc gcc gtc gac gac agc tgg tgc agg tgc gag gcg 288
Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala
85 90 95

atc agc cac atg ctg gga ggc atc tac agg gag ctc ggc gcc ccc gat 336
Ile Ser His Met Leu Gly Gly Ile Tyr Arg Glu Leu Gly Ala Pro Asp
100 105 110

gtc ggg cac ccc atg tcc gag gtg ttc cgc ggc tgc cgg aga ggg gac 384
Val Gly His Pro Met Ser Glu Val Phe Arg Gly Cys Arg Arg Gly Asp
115 120 125

ttg gag cgc gcg gcg gcg agc ctc ccg gcg ttc tgc aac gtg gac atc 432
Leu Glu Arg Ala Ala Ala Ser Leu Pro Ala Phe Cys Asn Val Asp Ile
130 135 140

ccc aac ggc gga ggt ggt gtc tgc tac tgg ctg gcg aga tct ggc tac 480
Pro Asn Gly Gly Gly Gly Val Cys Tyr Trp Leu Ala Arg Ser Gly Tyr
145 150 155 160

tag 483

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&lt;210&gt; 10

&lt;211&gt; 160

&lt;212&gt; PRT

<213> *Oryza sativa*

&lt;400&gt; 10

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Met Ala Ser Asn Lys Val Val Phe Ser Val Leu Leu Leu Ala Val Val
1 5 10 15
Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp
20 25 30
Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr
35 40 45
Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys
50 55 60
Val Gly Arg Gly Thr Ala Ala Ala Ala Glu Gln Val Arg Arg Asp Cys
65 70 75 80
Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala

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Ile	Ser	His	Met	Leu	Gly	Gly	Ile	Tyr	Arg	Glu	Leu	Gly	Ala	Pro	Asp
			100					105					110		
Val	Gly	His	Pro	Met	Ser	Glu	Val	Phe	Arg	Gly	Cys	Arg	Arg	Gly	Asp
		115					120					125			
Leu	Glu	Arg	Ala	Ala	Ala	Ser	Leu	Pro	Ala	Phe	Cys	Asn	Val	Asp	Ile
	130					135					140				
Pro	Asn	Gly	Gly	Gly	Gly	Val	Cys	Tyr	Trp	Leu	Ala	Arg	Ser	Gly	Tyr
145					150					155					160

&lt;210&gt; 11

&lt;211&gt; 707

&lt;212&gt; DNA

&lt;213&gt; Triticum durum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (27)..(533)

&lt;400&gt; 11

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agcgaaccag acttggttag aatacc atg gcg tgc aag tcc agc tgc agc ctc 53
                Met Ala Cys Lys Ser Ser Cys Ser Leu
                  1                      5

ctc ctc ttg gcc gcc gtc ctg ctc tcc gtc ttg gcc gct gct tcc gcc 101
Leu Leu Leu Ala Ala Val Leu Leu Ser Val Leu Ala Ala Ala Ser Ala
10                      15                      20                      25

tcc gcc agc tgc gtc cca ggg gtg gct ttt cgg acc aat ctt ctg cca 149
Ser Gly Ser Cys Val Pro Gly Val Ala Phe Arg Thr Asn Leu Leu Pro
                      30                      35                      40

cac tgc cgc gac tat gtg tta caa caa act tgt ggc acc ttc acc cct 197
His Cys Arg Asp Tyr Val Leu Gln Gln Thr Cys Gly Thr Phe Thr Pro
                      45                      50                      55

ggg tca aag tta ccc gaa tgg atg aca tct gcg tgc ata tac tcc cct 245
Gly Ser Lys Leu Pro Glu Trp Met Thr Ser Ala Ser Ile Tyr Ser Pro
                      60                      65                      70

ggg aaa ccg tac ctc gcc aag ttg tat tgc tgc cag gag ctc gca gaa 293
Gly Lys Pro Tyr Leu Ala Lys Leu Tyr Cys Cys Gln Glu Leu Ala Glu
                      75                      80                      85

att tct cag cag tgc cgg tgc gag gcg ctg cgc tac ttc ata gcg ttg 341
Ile Ser Gln Gln Cys Arg Cys Glu Ala Leu Arg Tyr Phe Ile Ala Leu
90                      95                      100                      105

ccg gta ccg tct cag cct gtg gac ccg agg tcc ggc aat gtt ggt gag 389
Pro Val Pro Ser Gln Pro Val Asp Pro Arg Ser Gly Asn Val Gly Glu
                      110                      115                      120

agc ggc ctc atc gat ctg ccc gga tgc ccc agg gag atg caa tgg gac 437
Ser Gly Leu Ile Asp Leu Pro Gly Cys Pro Arg Glu Met Gln Trp Asp
                      125                      130                      135

ttc gtc aga tta ctc gtc gcc ccg ggg cag tgc aac ttg gcg acc att 485
Phe Val Arg Leu Leu Val Ala Pro Gly Gln Cys Asn Leu Ala Thr Ile
140                      145                      150

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cac aat gtt cga tac tgc ccc gcc gtg gaa cag cct ctg tgg atc tag 533  
 His Asn Val Arg Tyr Cys Pro Ala Val Glu Gln Pro Leu Trp Ile  
 155 160 165

agataaaatc agtcgctcgt gaataagcat gcatgttgca tccataggcg tgtggtgtgc 593  
 atgtatacat atgtgagctc cgcgcgctca acatgtgtgg gctatctgct atgaatgaga 653  
 ataaagagaa tcattctgtg gttctttaat ttcaactaaa aaaaaaaaaa aaaa 707

<210> 12  
 <211> 168  
 <212> PRT  
 <213> Triticum durum

<400> 12  
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 20 25 30  
 Val Ala Phe Arg Thr Asn Leu Leu Pro His Cys Arg Asp Tyr Val Leu  
 35 40 45  
 Gln Gln Thr Cys Gly Thr Phe Thr Pro Gly Ser Lys Leu Pro Glu Trp  
 50 55 60  
 Met Thr Ser Ala Ser Ile Tyr Ser Pro Gly Lys Pro Tyr Leu Ala Lys  
 65 70 75 80  
 Leu Tyr Cys Cys Gln Glu Leu Ala Glu Ile Ser Gln Gln Cys Arg Cys  
 85 90 95  
 Glu Ala Leu Arg Tyr Phe Ile Ala Leu Pro Val Pro Ser Gln Pro Val  
 100 105 110  
 Asp Pro Arg Ser Gly Asn Val Gly Glu Ser Gly Leu Ile Asp Leu Pro  
 115 120 125  
 Gly Cys Pro Arg Glu Met Gln Trp Asp Phe Val Arg Leu Leu Val Ala  
 130 135 140  
 Pro Gly Gln Cys Asn Leu Ala Thr Ile His Asn Val Arg Tyr Cys Pro  
 145 150 155 160  
 Ala Val Glu Gln Pro Leu Trp Ile  
 165

<210> 13  
 <211> 712  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (33)..(500)

<400> 13  
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 Met Ala Ser Ser Ser Ser Ser  
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 agc cac cgc cgc ctc atc ctc gca gcc gcc gtc ctg ctc tcc gtg ctc 101  
 Ser His Arg Arg Leu Ile Leu Ala Ala Val Leu Leu Ser Val Leu  
 10 15 20

gcg gct gcc agc gcc agc gcc ggg acc tcc tgc gtg ccg ggg tgg gcc 149  
 Ala Ala Ala Ser Ala Ser Ala Gly Thr Ser Cys Val Pro Gly Trp Ala  
 25 30 35

atc ccg cac aac ccg ctc ccg agc tgc cgc tgg tac gtg acc agc cgg 197  
 Ile Pro His Asn Pro Leu Pro Ser Cys Arg Trp Tyr Val Thr Ser Arg  
 40 45 50 55

acc tgc ggc atc ggg ccg cgc ctc ccg tgg ccg gag ctg aag agg aga 245  
 Thr Cys Gly Ile Gly Pro Arg Leu Pro Trp Pro Glu Leu Lys Arg Arg  
 60 65 70

tgc tgc ccg gag ctg gcg gac atc ccg gcg tac tgc ccg tgc acg gcg 293  
 Cys Cys Arg Glu Leu Ala Asp Ile Pro Ala Tyr Cys Arg Cys Thr Ala  
 75 80 85

ctg agc atc ctc atg gac ggc gcg atc ccg cct ggc ccg gac gcg cag 341  
 Leu Ser Ile Leu Met Asp Gly Ala Ile Pro Pro Gly Pro Asp Ala Gln  
 90 95 100

ctg gag ggc cgc cta gag gac ctg ccg ggc tgc ccg ccg gag gtg cag 389  
 Leu Glu Gly Arg Leu Glu Asp Leu Pro Gly Cys Pro Arg Glu Val Gln  
 105 110 115

agg gga ttc gcc gcc acc ctc gtc acg gag gcc gag tgc aac ctg gcc 437  
 Arg Gly Phe Ala Ala Thr Leu Val Thr Glu Ala Glu Cys Asn Leu Ala  
 120 125 130 135

acc atc agc ggc gtc gcc gaa tgc ccc tgg att ctc ggc ggc gga acg 485  
 Thr Ile Ser Gly Val Ala Glu Cys Pro Trp Ile Leu Gly Gly Gly Thr  
 140 145 150

atg ccc tcc aag taa ctgcgaagag catagtgcac gaggaatgag cttgtagcta 540  
 Met Pro Ser Lys  
 155

gctcatatgt ctgaataata agcacagcaa gaagatgaat gcatttctcg gatcgttcat 600

ccggaacaat aattaaagg gatccggatt tgttcttgtg atataattaa cgattcctgt 660

tataacttga agtagctagg ctgcgtcccca tccaatgcaa gcaaaaaaaaa aa 712

<210> 14  
 <211> 155  
 <212> PRT  
 <213> Zea mays

<400> 14  
 Met Ala Ser Ser Ser Ser Ser Ser His Arg Arg Leu Ile Leu Ala Ala  
 1 5 10 15  
 Ala Val Leu Leu Ser Val Leu Ala Ala Ser Ala Ser Ala Gly Thr  
 20 25 30  
 Ser Cys Val Pro Gly Trp Ala Ile Pro His Asn Pro Leu Pro Ser Cys  
 35 40 45  
 Arg Trp Tyr Val Thr Ser Arg Thr Cys Gly Ile Gly Pro Arg Leu Pro  
 50 55 60  
 Trp Pro Glu Leu Lys Arg Arg Cys Cys Arg Glu Leu Ala Asp Ile Pro  
 65 70 75 80

Ala	Tyr	Cys	Arg	Cys	Thr	Ala	Leu	Ser	Ile	Leu	Met	Asp	Gly	Ala	Ile
				85					90					95	
Pro	Pro	Gly	Pro	Asp	Ala	Gln	Leu	Glu	Gly	Arg	Leu	Glu	Asp	Leu	Pro
			100					105					110		
Gly	Cys	Pro	Arg	Glu	Val	Gln	Arg	Gly	Phe	Ala	Ala	Thr	Leu	Val	Thr
		115				120						125			
Glu	Ala	Glu	Cys	Asn	Leu	Ala	Thr	Ile	Ser	Gly	Val	Ala	Glu	Cys	Pro
	130					135					140				
Trp	Ile	Leu	Gly	Gly	Gly	Thr	Met	Pro	Ser	Lys					
145					150					155					

```
<210> 15
<211> 122
<212> PRT
<213> Eleusine coracana
```

```

<400> 15
Ser Val Gly Thr Ser Cys Ile Pro Gly Met Ala Ile Pro His Asn Pro
  1              5              10              15
Leu Asp Ser Cys Arg Trp Tyr Val Ala Lys Arg Ala Cys Gly Val Gly
              20              25              30
Pro Arg Leu Ala Thr Gln Glu Met Lys Ala Arg Cys Cys Arg Gln Leu
          35              40              45
Glu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Val Arg Ile Leu Met
  50              55              60
Asp Gly Val Val Thr Pro Ser Gly Gln His Glu Gly Arg Leu Leu Gln
  65              70              75              80
Asp Leu Pro Gly Cys Pro Arg Gln Val Gln Arg Ala Phe Ala Pro Lys
              85              90              95
Leu Val Thr Glu Val Glu Cys Asn Leu Ala Thr Ile His Gly Gly Pro
          100              105              110
Phe Cys Leu Ser Leu Leu Gly Ala Gly Glu
  115              120

```

```
<210> 16
<211> 121
<212> PRT
<213> Secale cereale
```

```

<400> 16
Ser Val Gly Gly Gln Cys Val Pro Gly Leu Ala Met Pro His Asn Pro
  1                               5                               10                               15

Leu Gly Ala Cys Arg Thr Tyr Val Val Ser Gln Ile Cys His Val Gly
      20      .      .      25      30

Pro Arg Leu Phe Thr Trp Asp Met Lys Arg Arg Cys Cys Asp Glu Leu
      35      40      45

Leu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Leu Arg Ile Leu Met
  50      55      60

```

Asp Gly Val Val Thr Gln Gln Gly Val Phe Glu Gly Gly Tyr Leu Lys  
 65 70 75 80  
 Asp Met Pro Asn Cys Pro Arg Val Thr Gln Arg Ser Tyr Ala Ala Thr  
 85 90 95  
 Leu Val Ala Pro Gln Glu Cys Asn Leu Pro Thr Ile His Gly Ser Pro  
 100 105 110  
 Tyr Cys Pro Thr Leu Gln Ala Gly Tyr  
 115 120

<210> 17  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 17  
 accaataaac tagtatcaac aatggcatcc gacca 35

<210> 18  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 18  
 ccaacctttt ttattcatca atcgccaca 30

<210> 19  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 19  
 tcggattcca ttgcccagct atctgtc 27

<210> 20  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 20  
 atgggccta acaatcagta aattgaacg 29

<210> 21  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 21  
cgggtaccggc aggctgaagt cca

23

<210> 22  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 22  
ccggggatct accatgagcc caga

24

<210> 23  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 23  
gaatgaaccg aaaccggcgg ta

22

<210> 24  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 24  
taccacctcc ctgaggtttg

20

<210> 25  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 25  
ccatgcctag ggtcacactt

20